

NEO-EPITOPE PREDICTION EXERCISE – ANSWERS

IMMUNOLOGICAL BIOINFORMATICS 2016

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Q1. Nucleotide alteration for the first five variant calls

G/A
C/T
C/T
G/A
C/T

Q2. Where to find allele-frequency in a VCF file, for both tumor and normal sample

```
padawan[ambj]:/home/people/ambj/ImmunoBioinf/data> grep 'Allele fraction'
MEL1.vcf
##FORMAT=<ID=AF,Number=1,Type=Float,Description="Allele fraction of the
event in the tumor">
```

Column 9 FORMAT (Third, colon separated)

Column 10 TUMOR

Column 11 NORMAL

CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	TUMOR	NORMAL
Chr1	971916	.	G	A	.	PASS	ECNT=1; HCNT=1; MAX_ED=.; MIN_ED=.; NLOD=10.53; TLOD=10.51	GT: AD: AF: ALT_F1R2: ALT_F2R1: FOXOG: QSS: REF_F1R2: REF_F2R1	0/1: 12,4: 0.250: 3: 1: 0.750: 397,127: 8: 4	0/0: 35,0: 0.00: 0: 0: .: 1174,0: 22: 13

Q3. Genes: 403, Transcripts: 1181

Q4. 3970 unique peptides

Q5. 74 mutated peptides have a percent rank score of 2 or lower when binding is predicted for HLA-A*02:01.

Q6. 3 peptides originates from frameshift mutations

HLA_allele	Norm peptide	Mut peptide	Mut MHCrank	Mutation Consequence	Priority Score
HLA-A02:01FIV..	LMFTWQNSA	0.8	F	20
HLA-A02:01	C...L...A	FTWQNSALL	1.5	F	21
HLA-A02:01P.G.S	HLQGEAYAV	2	F	2

Q7. Alanine (A) : HLYASLSRA → HLYASLSRV

Q8. Immunogenic peptides

HLA_allele	Norm_peptide	Mut_peptide	priority_Score
HLA-A02:01Q..	IILVAVPHV	20
HLA-A02:01	.P.....	HLYASLSRA	7
HLA-A02:01R.....	MLGEQLFPL	13

Q9. The priority score for the anchor optimized peptide is 14

Q10. There are 48 peptides with a priority score higher the nor equal to 13 (lowest immunogens peptides priority score)